

SEQUENCE LISTING

5 <110> Syngenta Biotechnology, Inc.  
Grina, Jonas

<120> NOVEL CYANOENAMINES USEFUL AS LIGANDS FOR MODULATING GENE EXPRESSION  
IN PLANTS OR ANIMALS

10 <130> 1392/2/2

<150> 60/272,905

15 <151> 2001-03-02

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 17

<212> DNA

<213> synthetic construct

<220>

<221> misc\_feature

<222> (1)..(17)

<223>

40 <400> 1  
agcttgaggg tataatg 17

<210> 2

45 <211> 17

<212> DNA

<213> synthetic construct

50 <220>

<221> misc\_feature

55 <222> (1)..(17)

<223>

<400> 2  
actcccatat tactcga 17

5

<210> 3

<211> 36

10

<212> DNA

<213> synthetic construct

15

<220>

<221> misc\_feature

<222> (1)..(36)

20

<223>

<400> 3  
gatccgagac aagggttcaa tgcacttgtc caatga 36

25

<210> 4

<211> 36

30

<212> DNA

<213> synthetic construct

35

<220>

<221> misc\_feature

<222> (1)..(36)

40

<223>

<400> 4  
gctctgttcc caagttacgt gaacagggtta ctctag 36

45

<210> 5

<211> 147

50

<212> DNA

<213> synthetic construct

55

<220>

<221> misc\_feature

<222> (1)..(147)

5 <223> sequence in the inserted region of pCGS154

<400> 5

gatccgagac aagggttcaa tgcacttgtc caatgagatc cgagacaagg gttcaatgca 60

10 cttgtccaat gagatctcat tggacaagtg cattgaacct tgtctcggat ctcatgggac 120

aagtgcattg aacccttgtc tcggatc 147

15 <210> 6

<211> 2840

<212> DNA

<213> Manduca sexta

<220>

<221> CDS

<222> (361)..(2031)

<223> Manduca sexta Ecdysone Receptor

<400> 6

tccgttgacg acggtcgcac gcgtgcaacg tgctcgtttt tacgggtcaa gcgaacgcgt 60

aacctccgtc tccacatcac cgagcgaact ctagaactcg cgtactcttc tcacctgttg 120

cttcggattg tgttgtgact gaaaagcgac gcgtatcgtg gtcgaagatt ctctataagt 180

gcataatata ttcgagacag tggatagcga ttcgtttcgg tttcatcgcg cggatgagtg 240

40 gttcatgccc gtagagacgc gtttagatag ttatggcgag gaaaaagtga agtgaaagcc 300

tacgtcagag gatgtccctc ggtggtcacg gaagccgggg cgtgtgacgc gctcttcgac 360

atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt 408

45 Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe  
1 5 10 15

gag gag agc tcc tct gaa gtg act tct tcc tcg gcg ttc ggg atg ccg 456

50 Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Ala Phe Gly Met Pro  
20 25 30

gcg gcc atg gta atg tca ccg gag tcg ctg gcg tcg cca gag tac ggc 504

Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly  
35 40 45

55

	ggc ctc gag ctc tgg agc tac gat gag acc atg aca aac tat ccg gcg	552
	Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala	
	50 55 60	
5	cag tca ctg ctc ggc gcg tgt aat gcg ccg cag cag cag cag caa cag	600
	Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln Gln	
	65 70 75 80	
10	caa caa cag cag ccg tcc gct cag ccg ctg ccg tct atg ccg ctg ccg	648
	Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro	
	85 90 95	
15	atg cct cct aca act cct aaa tca gag aac gag tcc atg tgc tca ggt	696
	Met Pro Pro Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly	
	100 105 110	
20	cga gaa gaa tta tca ccg gcc tca agt ata aat gga tgt agt act gat	744
	Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp	
	115 120 125	
25	ggg gaa cca aga cga cag aag aaa ggg cca gcg ccg cgc cag cag gag	792
	Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu	
	130 135 140	
30	gaa ctg tgc ctt gtt tgc ggc gac agg gct tgc gga tat cac tat aac	840
	Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn	
	145 150 155 160	
35	gcg ctt acg tgc gaa gga tgt aaa ggg ttc ttc agg cgg agt gtg acc	888
	Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr	
	165 170 175	
40	aag aat gcg gta tat att tgt aaa ttt gga cac gcc tgc gag atg gac	936
	Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp	
	180 185 190	
45	atg tac atg agg aga aaa tgc caa gag tgt cgg ttg aag aaa tgc ctc	984
	Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu	
	195 200 205	
50	gcg gtg ggc atg agg ccc gag tgc gtc gtc cca gag tcc acg tgc aag	1032
	Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys	
	210 215 220	
55	aac aaa aga aga gaa aag gaa gca cag aga gaa aaa gac aaa ctg cca	1080
	Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro	
	225 230 235 240	
60	gtc agt acg acg aca gtg gac gat cat atg cct gcc ata atg caa tgt	1128
	Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys	
	245 250 255	
65	gac cct ccg ccc cca gag gcg gca agg att cac gaa gtg gtc ccg agg	1176
	Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg	
	260 265 270	

	ttc cta acg gag aag cta atg gag cag aac aga ctg aag aat gtg acg	1224
	Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr	
	275 280 285	
5	ccg ctg tcg gcg aac cag aag tcc ctg atc gcg agg ctc gtg tgg tac	1272
	Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr	
	290 295 300	
10	cag gag ggg tac gag cag ccg tcg gag gaa gat ctc aag aga gtt aca	1320
	Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr	
	305 310 315 320	
15	cag aca tgg cag tta gaa gaa gaa gaa gag gag gaa act gac atg ccc	1368
	Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro	
	325 330 335	
20	ttc cgt cag atc aca gag atg acg atc tta aca gtg cag ctt att gta	1416
	Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val	
	340 345 350	
25	gaa ttc gca aag gga cta ccg gga ttc tcc aag ata tct cag tcc gat	1464
	Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp	
	355 360 365	
30	caa att aca tta tta aag gcg tca tca agc gaa gtg atg atg ctg cga	1512
	Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg	
	370 375 380	
35	gtg gcg cga cgg tac gac gcg gcg acg gac agc gtg ctg ttc gcg aac	1560
	Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn	
	385 390 395 400	
40	aac cag gcg tac acg cgc gac aac tac cgc aag gcg ggc atg tcc tac	1608
	Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr	
	405 410 415	
45	gtc atc gag gac ctg ctg cac ttc tgt cgg tgt atg tac tcc atg agc	1656
	Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser	
	420 425 430	
50	atg gac aat gtg cac tac gcg ctg ctc acc gcc atc gtt ata ttc tca	1704
	Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser	
	435 440 445	
55	gac cgg cca ggc ctc gag caa ccc ctt tta gtg gag gaa atc cag aga	1752
	Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg	
	450 455 460	
60	tac tac ttg aag acg ctg cgg gtt tac att tta aat cag cac agc gcg	1800
	Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala	
	465 470 475 480	
65	tcg cct cgc tgc gcc gtg ctg ttc ggc aag atc ctc ggc gtg ctg acg	1848
	Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr	
	485 490 495	

	gaa ctg cgc acg ctc ggc acg cag aac tcc aac atg tgc atc tcg ctg	1896
	Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu	
	500 505 510	
5	aag ctg aag aac agg aaa ctt ccg cca ttc ctc gag gag atc tgg gac	1944
	Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp	
	515 520 525	
10	gtg gcc gaa gtg tcg acg acg cag ccg acg ccg ggg gtg gcg gcg cag	1992
	Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln	
	530 535 540	
15	gtg acc ccc atc gtg gtg gac aac ccc gcg gcg ctc tag ctggcgcgcc	2041
	Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu	
	545 550 555	
	ggcgcgcgcg cccgcgcgcc ccgcgcgcgc cgctcccccg cgccgcgcgc gcgcgcgcgc	2101
	gcggcgctgcg ctgagtgcgg gacccgcccc gaggagagaa cgctcataga ctggctagtt	2161
20	ttagtgaagt gcacggacgc gatcgtggga ccgcatcgac gcgtccgtga ggacagtgca	2221
	aatattaccg ctagggccgg ttcgtacgtg tccggtgacc gacgacgatg atgcgcgtga	2281
25	gattagtga tatatgtgtt gttgaacgtt tggagagtat atttagtgtt gatcgtcggg	2341
	agcgcgcggc cggcgcggtg cggcgagctg tccgcgcgcg gccggccgcg gcgactccgc	2401
30	gtttttttcg tttgcgaccg gaaaccgagt cggtcactcg gatacgcccg tatgataaga	2461
	cttcttttga taaataagtt cacctgtatt gcgcgtacat acgagaatta taaagaaaaa	2521
	aagtaataata tgaagagatg tttctattgg gtgaaaagtt taaacttatg tttatttacc	2581
35	aaaattaact atacgttgat cgaccttttg actataatat tgtgctgggt cgttggcagc	2641
	ggccgacgaa cgcgcgcgca ccatatttgt ttatatatag tttatgtgag acgttatcgt	2701
40	gtcgtgtcca cttagttccg attcatgttc caccaggtcg gtgtagtgat cagggcgggc	2761
	caggggtgacg gccaccacgg ataacaggca aagagcgacg aatgttttca tgttgagact	2821
	ttgggagacg ttattcctc	2840
45	<210> 7	
	<211> 556	
50	<212> PRT	
	<213> Manduca sexta	
	<400> 7	
55	Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe	
	1 5 10 15	

	Glu	Glu	Ser	Ser	Ser	Glu	Val	Thr	Ser	Ser	Ser	Ala	Phe	Gly	Met	Pro	
				20					25					30			
5	Ala	Ala	Met	Val	Met	Ser	Pro	Glu	Ser	Leu	Ala	Ser	Pro	Glu	Tyr	Gly	
			35					40					45				
	Gly	Leu	Glu	Leu	Trp	Ser	Tyr	Asp	Glu	Thr	Met	Thr	Asn	Tyr	Pro	Ala	
		50					55					60					
10	Gln	Ser	Leu	Leu	Gly	Ala	Cys	Asn	Ala	Pro	Gln	Gln	Gln	Gln	Gln	Gln	
	65					70				75						80	
	Gln	Gln	Gln	Gln	Pro	Ser	Ala	Gln	Pro	Leu	Pro	Ser	Met	Pro	Leu	Pro	
15					85					90					95		
	Met	Pro	Pro	Thr	Thr	Pro	Lys	Ser	Glu	Asn	Glu	Ser	Met	Ser	Ser	Gly	
				100					105					110			
20	Arg	Glu	Glu	Leu	Ser	Pro	Ala	Ser	Ser	Ile	Asn	Gly	Cys	Ser	Thr	Asp	
			115					120					125				
	Gly	Glu	Pro	Arg	Arg	Gln	Lys	Lys	Gly	Pro	Ala	Pro	Arg	Gln	Gln	Glu	
		130					135					140					
25	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn	
						150					155					160	
	Ala	Leu	Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Val	Thr	
30					165					170					175		
	Lys	Asn	Ala	Val	Tyr	Ile	Cys	Lys	Phe	Gly	His	Ala	Cys	Glu	Met	Asp	
			180						185					190			
35	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	
			195					200					205				
	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Ser	Thr	Cys	Lys	
		210					215					220					
40	Asn	Lys	Arg	Arg	Glu	Lys	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Leu	Pro	
	225					230					235					240	
	Val	Ser	Thr	Thr	Thr	Val	Asp	Asp	His	Met	Pro	Ala	Ile	Met	Gln	Cys	
45					245					250					255		
	Asp	Pro	Pro	Pro	Pro	Glu	Ala	Ala	Arg	Ile	His	Glu	Val	Val	Pro	Arg	
				260				265						270			
50	Phe	Leu	Thr	Glu	Lys	Leu	Met	Glu	Gln	Asn	Arg	Leu	Lys	Asn	Val	Thr	
			275					280					285				
	Pro	Leu	Ser	Ala	Asn	Gln	Lys	Ser	Leu	Ile	Ala	Arg	Leu	Val	Trp	Tyr	
		290					295					300					
55	Gln	Glu	Gly	Tyr	Glu	Gln	Pro	Ser	Glu	Glu	Asp	Leu	Lys	Arg	Val	Thr	
	305					310					315					320	

5 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro  
 325 330 335  
 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val  
 340 345 350  
 10 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp  
 355 360 365  
 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg  
 370 375 380  
 15 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn  
 385 390 395 400  
 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr  
 405 410 415  
 20 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser  
 420 425 430  
 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser  
 435 440 445  
 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg  
 450 455 460  
 30 Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala  
 465 470 475 480  
 Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr  
 485 490 495  
 35 Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu  
 500 505 510  
 40 Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp  
 515 520 525  
 Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln  
 530 535 540  
 45 Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu  
 545 550 555  
 <210> 8  
 50 <211> 30  
 <212> DNA  
 55 <213> synthetic construct



<220>

<221> misc\_feature

5 <222> (1)..(30)

<223>

<400> 8

10 ggatcctaaa gcttcgtcgt cgacacttcg 30

<210> 9

15 <211> 30

<212> DNA

<213> synthetic construct

20

<220>

<221> misc\_feature

25 <222> (1)..(30)

<223>

<400> 9

30 ggatccatgg gycgagaaga attrtcacccr 30

<210> 10

35 <211> 21

<212> DNA

<213> synthetic construct

40

<220>

<221> misc\_feature

45 <222> (1)..(21)

<223>

<400> 10

50 ccacrtccca gatctcctcg a 21

<210> 11

55 <211> 19

<212> DNA

<213> synthetic construct

5 <220>

<221> misc\_feature

<222> (1)..(19)

10 <223>

<400> 11  
aagcttgccc ccccgaccg 19

15

<210> 12

<211> 25

20 <212> DNA

<213> synthetic construct

25 <220>

<221> misc\_feature

<222> (1)..(25)

30 <223>

<400> 12  
tctagaggat cctacccacc gtact 25

35